

Amendments to the Specification

Please replace the second full paragraph on page 32 with the following amended paragraph:

These and other embodiments are disclosed or are obvious from and encompassed by the description and examples of the present invention. Further literature concerning any one of the methods, uses and compounds to be employed in accordance with the present invention may be retrieved from public libraries, using for example electronic devices. For example the public database "Medline" may be utilized which is available on the Internet, e.g. under ~~<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>~~. Further databases and addresses, such as ~~<http://www.ncbi.nlm.nih.gov/>, <http://www.infobiogen.fr/>, http://www.fmi.ch/biology/research_tools.html, <http://www.tigr.org/>~~, are known to the person skilled in the art and can also be obtained using, e.g., ~~<http://www.lycos.com>~~ the PubMed website, the NCBI website, the InfoBiogen website, the Institute for Genomic Research (TIGR) website, and the lycos website. An overview of patent information in biotechnology and a survey of relevant sources of patent information useful for retrospective searching and for current awareness is given in Berks, TIBTECH 12 (1994), 352-364.

Please replace Table 1 on page 39 with the following amended Table 1:

Name	Position	Sequence (5' - 3')	<u>Sequence Identifier</u>
T7	BAC CS	TAATACGACTCACTATAGGG	<u>SEQ ID NO:1</u>
3A43F	exon 2	GAACCCATTCACATGGAC	<u>SEQ ID NO:2</u>
3A46R	exon 4	TGATCATGTCAGGATCTG	<u>SEQ ID NO:3</u>

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3A47F	exon 4	GGTCAACAGCCTGTGCTG	<u>SEQ ID NO:4</u>
3A48R	exon 5	TCCACTGGTGAAGGTTGG	<u>SEQ ID NO:5</u>
3A49F	exon 5	GTGCCATCTCTATAGCTG	<u>SEQ ID NO:6</u>
3A410R	exon 6	CTTCCCGCCTCAGATTC	<u>SEQ ID NO:7</u>
3A411F	exon 6	GAAATCTGAGGCGGGAAG	<u>SEQ ID NO:8</u>
3A412R	exon 7	GGGTCTTGTGGATTGTTG	<u>SEQ ID NO:9</u>
3A413F	exon 7	CAACAATCCACAAGACCC	<u>SEQ ID NO:10</u>
3A414R	exon 8	GTGTATCTTCGAGGCGAC	<u>SEQ ID NO:11</u>
3A415F	exon 8	CTTCCATTCCTCATCCC	<u>SEQ ID NO:12</u>
3A416R	exon 9	CCTTTGTGGGACTCAGTTTC	<u>SEQ ID NO:13</u>
3A419F	exon 10	GCCACTCACCTGATGTC	<u>SEQ ID NO:14</u>
3A720R	exon 11	ATCACCACCCACCCTTG	<u>SEQ ID NO:15</u>
3A721F	exon 11	CAAAGGGTGGGTGGTGAT	<u>SEQ ID NO:16</u>
3A422R	exon 12	GAGAGCAAACCTCATGCC	<u>SEQ ID NO:17</u>
3A423F	exon 12	GGCATGAGGTTTGCTCTC	<u>SEQ ID NO:18</u>
3A424R	exon 13	GGTGCCATCCCTTGACTC	<u>SEQ ID NO:19</u>
3A426R	exon 2	GCAGAGGTGTGGGCCCTG	<u>SEQ ID NO:20</u>
3A4436F	intron 8	GGAGATCAAGGACCACGCTTGTG	<u>SEQ ID NO:21</u>
3A441R	intron 10	CTTACGCTTCTGCCAGTAGCAACC	<u>SEQ ID NO:22</u>
CYP3A4PF	promoter	AACAGGCGTGGAACACAAT	<u>SEQ ID NO:23</u>
CYP3A4PR	promoter	CTTTCCTGCCCTGCACAG	<u>SEQ ID NO:24</u>

Please replace Table 2 on page 41 with the following amended Table 2:

Exon	Primer name	Primer sequence (5' - 3' orientation)	Location on BAC 22300	Fragment length	Annealing Temp.	SEQ ID NO:
1	3 ^a 4-62F	AACTGCAGGCAGAGCACAGGT	61838 - 61858	384 bp	63°C	<u>25</u>
	3A4-64R	CCACGCCCCGGCCTGAACATCT	62221 - 62201			<u>26</u>
2 ^a	3A4-101F	TAGGATCCAATCATCTCCTAC	65072 - 65092	463 bp	62°C	<u>27</u>
	3A4-68F	GGTGTCTCATGGTGGAGG	65841 - 65858			<u>28</u>
	3A4-103R	AGAGTTAGCAAGAGAGCCCTT	66303 - 66283			<u>29</u>

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3	3A4-50F	CCTCTAACTGCCAGCAAGTCTG	67924 - 67945	249 bp	58°C	<u>30</u>
	3A4-51R	GCGCTGAGACTGTCCTCTGTG	68172 - 68152			<u>31</u>
4 ^b	3A4-52F	AGTCTGGCTTCCTGGGTTGGGCTC	73343 - 73366	293 bp	58°C	<u>32</u>
	3A4-37R	GAAGTGGACGTGGAACCTTCCTGGAC	73635 - 73610			<u>142</u>
	3A4-100R	GGGGACAGGATGAAGTGGACG	73646 - 73626	304 bp	63°C	<u>33</u>
5	3A4-28F	TACAACCATGGAGACCTCC	75813 - 75832	236 bp	62°C	<u>34</u>
	3A4-29R	TACCTGTCCCCACCAGATTC	76048 - 76029			<u>35</u>
6	3A4-57F	CCCTTTCCAAGGGGTAGTCC	76066 - 76085	379 bp	58°C	<u>36</u>
	3A4-32R	GTCTGGTCACTGGAATAACCCAACAGC AGG	76444 - 76415			<u>37</u>
7	3A4-33F	GTCTGTCTTGACTGGACATGTGG	77509 - 77531	393 bp	58°C	<u>38</u>
	3A4-34R	GATGATGGTCACACATATCTTC	77901 - 77880			<u>39</u>
8	3A4-35F	GGCTTCCAGTTGAGAACCTTGATGTC	78723 - 78748	389 bp	58°C	<u>40</u>
	3A4-59R	GCTCTAAACATGAGCAGTCTTC	79111 - 79090			<u>41</u>
9	3A4-36F	GGAGATCAAGGACCACGCTTGTC	79584 - 79606	240 bp	62°C	<u>42</u>
	3A4-47R	CTCATCATCCTGGAATACTTCCTGC	79823 - 79799			<u>43</u>
10	3A4-82F	CCCAGTGACCTCTGAATTGC	81959 - 81979	431 bp	50°C	<u>44</u>
	3A4-95R	CAGAGCCTTCCTACATAG	82389 - 82372			<u>45</u>
11	3A4-97F	CAGTATGAGTTAGTCTCTGG	83733 - 83752	574 bp	50°C	<u>46</u>
	3A4-80R	CATAACTGATGACCTTCATCG	84306 - 84286			<u>47</u>
12	3A4-49F	CCTGTGTACTGCTAGTAGAGGG	85020 - 85041	411 bp	50°C	<u>48</u>
	3A4-39R	CACAGATGGGCCTAATTG	85430 - 85413			<u>49</u>
13	3A4-48F	GGAGTGTCTCACTCACTTTGATGC	87799 - 87822	288 bp	50°C	<u>50</u>
	3A4-25R	TGGATGAAGCCCATCTTC	88086 - 88069			<u>51</u>
11	3A7-42F	CCAGTATGAGTTGTTCTCTGG	87799 - 87822	404 bp	58°C	<u>140</u>
	3A7-38R	AGGCAGAATATGCTTGAACCAGGC	88086 - 88069			<u>141</u>

Please replace Table 3 on page 43 with the following amended Table 3:

Nr	Variant ^b	Nucleotide sequence (5'-3')	Genetic element	Predicted effect	N ^c	Heterozygotes found (%)	Homozygotes found (%)	Homozygotes calculated (%)	Variant allele frequency (%)	SEQ ID NO: (* = reverse complement)
M1	g.6004G>A	TCCACAGGGCTTTTGTA.....	Exon 3	G56D	426	2,82	0,00	0,0190	1,41	<u>52</u> <u>54</u> <u>55</u>
M2	g.13908G>A	ATTACGATCATA.....	Exon 5	R130Q	300	0,66	0,00	0,0011	0,33	<u>60</u> <u>62</u> <u>63</u>
M3	g.14292G>A	AGCCTGTCACCA.....	Exon 6	V170I	424	0,47	0,00	0,0006	0,24	<u>64</u> <u>66</u> <u>67</u>
M4	g.14304G>C	TGAAACACAGTAAG.....	Exon 6	D174H	424	0,47	0,00	0,0006	0,24	<u>68</u> <u>70</u> <u>71</u>
M10	g.14323C>T	GCAGCCATGGGT.....	Intron 6		424	0,47	0,00	0,0006	0,24	<u>72</u> <u>74</u> <u>75</u>
M11	g.14329G>T	ATGGGGTTCTGT.....	Intron 6		424	0,47	0,00	0,0006	0,24	<u>76</u> <u>78</u> <u>79</u>
M12	g.14357T>G	CCAGCTGCCTGG.....	Intron 6		424	1,89	0,00	0,009	0,94	<u>80</u> <u>82</u> <u>83</u>
M13	g.15753T>G	TATCTTCTCTCTTG.....	Intron 7		296	5,41	0,00	0,073	2,70	<u>56</u> <u>58</u> <u>59</u>
M14	g.20230G>A	GGATGGTACATA.....	Intron 10		296	17,56	0,68	0,895	9,46	<u>84</u> <u>86</u> <u>87</u>
M5	g.21867C>T	TGAAACGCTCAT.....	Exon 11	T363M	298	0,67	0,00	0,001	0,34	<u>88</u> <u>90</u> <u>91</u>
M15	g.21868G>A	GAAACGCTCAGA.....	Exon 11	Silent	298	0,67	0,00	0,001	0,34	<u>92</u> <u>94</u> <u>95</u>
M6	g.21896C>T	TGAGACTTGAGT.....	Exon 11	L373F	298	0,67	0,00	0,001	0,34	<u>96</u> <u>98</u> <u>99</u>
M7	g.22026C>T	CCTCCCTGAAAT.....	Exon 11	P416L	298	0,67	0,00	0,001	0,34	<u>100</u> <u>102</u> <u>103</u>
M16	g.22041C>T	CAAGGCCCTGT.....	Intron 11		298	0,67	0,00	0,001	0,34	<u>104</u> <u>106</u> <u>109</u>
M17	g.23081C>T	ACCAACGTGGAT.....	Intron 11		426	0,47	0,00	0,001	0,23	<u>108</u> <u>110</u> <u>111</u>
M8	g.23172T>C	TGGCATGAGGTC.....	Exon 12	M445T	426	0,94	0,00	0,002	0,47	<u>112</u> <u>114</u> <u>115</u>
M18	g.25925C>T	GGCACCGTAAGT.....	Exon 13	Silent	300	0,66	0,00	0,001	0,33	<u>116</u> <u>118</u> <u>119</u>
M19	g.25958T>G	ACTTCTGCTTTG.....	3'UTR		300	0,66	0,00	0,001	0,33	<u>120</u> <u>122</u> <u>123</u>